

1 **Supplementary Material Hardy-Weinberg Equilibrium**

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4 Briefly, in the case of a single locus with two alleles (A and S) where p is the allele frequency of the dominant

5 allele, q is the frequency of the recessive allele (HbA and HbS respectively in the present study) and $p+q=1$,

6 genotype frequencies assuming HWE are equivalent to p^2 for homozygous dominants (AA), $2pq$ for

7 heterozygotes (AS), q^2 for homozygous recessives (SS) and $p^2+2pq+q^2=1$ (Equation 1). Considering a three-

8 allele case (for example HbA, HbS and HbC), the corresponding equation is $p^2+2pq+q^2+2pr+r^2+2qr=1$

9 (Equation 2) where r is the third allele (i.e. r^2 , $2pr$ and $2qr$ are CC, AC and SC proportions respectively).

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11 **Equation 1:** $p^2 + 2pq + q^2 = 1$

12 *where p and q are the proportions of the two alleles (e.g. HbA and HbS).*

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14 **Equation 2:** $p^2 + 2pq + q^2 + 2pr + r^2 + 2qr = 1$

15 *where p , q and r are the proportions of the three alleles (HbA, HbS and HbC).*

16 For each study population, we calculated the expected genotype frequencies based on these equations

17 (Table 1). Radar charts, created with a slightly modified version of the radarchart function included in the

18 “fmsb” package in R (see code in the Supplementary Information),⁸² are used to illustrate the relative

19 differences between observed and expected genotype counts for selected studies (Figure 2).